SEQUENCE LISTING

<110> Gao, Zeren
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Piddington, Christopher S.
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Shoemaker, Kimberly E.
Gilbertson, Debra G.
West, James W.

<120> GROWTH FACTOR HOMOLOG ZVEGF3

<130> 98-60C1

<160> 50

<170> FastSEQ for Windows Version 3.0

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<222> (154)...(1191)

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agtgcagcct tcccctggcg gtggtgaaag agactcggga gtcgctgctt ccaaagtgcc     120
cgccgtgagt gagctctcac cccagtcagc caa atg agc ctc ttc ggg ctt ctc      174
                                     Met Ser Leu Phe Gly Leu Leu
                                      1               5

ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa      222
Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu
        10                  15                  20

tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac      270
Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn
    25                  30                  35
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gga gta caa gat cct cag cat gag aga att att act gtg tct act aat      318
Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn
 40                  45                  50                  55

gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg      366
Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr
                 60                  65                  70

gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa      414
Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln
             75                  80                  85

ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata      462
Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile
         90                  95                 100

tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata      510
Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile
    105                 110                 115

tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct      558
Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
120                 125                 130                 135

aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct      606
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro
                140                 145                 150

tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc      654
Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe
            155                 160                 165

aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg      702
Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu
        170                 175                 180

gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt      750
Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu
    185                 190                 195
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att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta       798
Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu
200                 205                 210                 215

tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga       846
Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg
                220                 225                 230

aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta       894
Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu
            235                 240                 245

tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta       942
Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu
        250                 255                 260

aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc       990
Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg
    265                 270                 275

tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa      1038
Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln
280                 285                 290                 295

tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg      1086
Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu
                300                 305                 310

aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg      1134
Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val
            315                 320                 325

gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca      1182
Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr
        330                 335                 340

gga gga tag ccgcatcacc accagcagct cttgcccaga gctgtgcagt              1231
Gly Gly  *
    345

gcagtggctg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt   1291
gcttcaagga cctttcatct tcaggattta cagtgcattc tgaaagagga gacatcaaac   1351
agaattagga gttgtgcaac agctcttttg agaggaggcc taaaggacag gagaaaaggt   1411
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cttcaatcgt ggaaagaaaa ttaaatgttg tattaaatag atcaccagct agtttcagag   1471
ttaccatgta cgtattccac tagctgggtt ctgtatttca gttctttcga tacggcttag   1531
ggtaatgtca gtacaggaaa aaaactgtgc aagtgagcac ctgattccgt tgccttgctt   1591
aactctaaag ctccatgtcc tgggcctaaa atcgtataaa atctggattt tttttttttt   1651
tttttgctca tattcacata tgtaaaccag aacattctat gtactacaaa cctggttttt   1711
aaaaaggaac tatgttgcta tgaattaaac ttgtgtcgtg ctgatagga                1760

<210> 2
<211> 345
<212> PRT
<213> Homo sapiens

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Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
            20                  25                  30
Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
        35                  40                  45
Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
    50                  55                  60
His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
65                  70                  75                  80
Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
                85                  90                  95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
            100                 105                 110
Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
        115                 120                 125
Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
    130                 135                 140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                 150                 155                 160
Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
                165                 170                 175
Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
            180                 185                 190
Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
        195                 200                 205
Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
    210                 215                 220
Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225                 230                 235                 240
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Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
245 250 255
Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
260 265 270
Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
275 280 285
His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
290 295 300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
305 310 315 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
325 330 335
Cys Val Cys Arg Gly Ser Thr Gly Gly
340 345

<210> 3
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT
<222> (2)...(19)
<223> Xaa is any amino acid

<221> VARIANT
<222> (20)...(34)
<223> Xaa is any amino acid or not present

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<222> (94)...(113)
<223> Xaa is any amino acid not present

<221> VARIANT
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Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110
Xaa Cys Xaa Cys
115

<210> 4
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT

<222> (2)...(2)
<223> Xaa is Lys or Arg

<221> VARIANT
<222> (4)...(4)
<223> Xaa is Asp, Asn or Glu

<221> VARIANT
<222> (5)...(5)
<223> Xaa is Trp, Tyr or Phe

<221> VARIANT
<222> (6)...(16)
<223> Xaa is any amino acid

<221> VARIANT
<222> (17)...(20)
<223> Xaa is any amino acid or not present

<221> VARIANT
<222> (22)...(22)
<223> Xaa is Lys or Arg

<221> VARIANT
<222> (23)...(23)
<223> Xaa is Trp, Tyr or Phe

<400> 4
Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5   10   15
Xaa Xaa Xaa Xaa Gly Xaa Xaa Cys
            20

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide tag

<400> 5
Glu Tyr Met Pro Met Glu

1 5

<210> 6
<211> 1035
<212> DNA
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gtncargayc cncarcayga rmgnathath acngtnwsna cnaayggnws nathcaywsn     180
ccnmgnttyc cncayacnta yccnmgnaay acngtnytng tntggmgnyt ngtngcngtn     240
gargaraayg tntggathca rytnacntty gaygarmgnt tyggnytnga rgayccngar     300
gaygayatht gyaartayga yttygtngar gtngargarc cnwsngaygg nacnathytn     360
ggnmgntggt gyggnwsngg nacngtnccn ggnaarcara thwsnaargg naaycarath     420
mgnathmgnt tygtnwsnga ygartaytty ccnwsngarc cnggnttytg yathcaytay     480
aayathgtna tgccncartt yacngargcn gtnwsnccnw sngtnytncc nccnwsngcn     540
ytnccnytng ayytnytnaa yaaygcnath acngcnttyw snacnytnga rgayytnath     600
mgntayytng arccngarmg ntggcarytn gayytngarg ayytntaymg nccnacntgg     660
carytnytng gnaargcntt ygtnttyggn mgnaarwsnm gngtngtnga yytnaayytn     720
ytnacngarg argtnmgnyt ntaywsntgy acnccnmgna ayttywsngt nwsnathmgn     780
gargarytna armgnacnga yacnathtty tggccnggnt gyytnytngt naarmgntgy     840
ggnggnaayt gygcntgytg yytncayaay tgyaaygart gycartgygt nccnwsnaar     900
gtnacnaara artaycayga rgtnytncar ytnmgnccna aracnggngt nmgnggnytn     960
cayaarwsny tnacngaygt ngcnytngar caycaygarg artgygaytg ygtntgymgn    1020
ggnwsnacng gnggn                                                     1035
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<210> 7
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<213> Artificial Sequence

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<223> n = A,T,C or G

<400> 7
mgntgyggng gnaaytg 17

<210> 8
<211> 17
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<221> misc_feature
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<223> n = A,T,C or G

<400> 8
mgntgydsng gnwrytg 17

<210> 9
<211> 17
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<221> misc_feature
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<223> n = A,T,C or G

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carywnccns hrcanck 17

<210> 10
<211> 17
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<223> Oligonucleotide primer

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<223> n = A,T,C or G

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ttytggccng gntgyyt 17

<210> 11
<211> 17
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<221> misc_feature
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<223> n = A,T,C or G

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ntnddnccnn sntgybt 17

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<221> misc_feature
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<223> n = A,T,C or G

<400> 12
avrcansnng gnhhnan 17

<210> 13
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<220>
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<400> 13
caygargart gygaytg 17

<210> 14
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<220>
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<221> misc_feature
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<223> n = A,T,C or G

<400> 14
caynnnnvnt gyvvntg 17

<210> 15
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<221> misc_feature
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canbbrcanb nnnnrtg 17

<210> 16
<211> 17
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<223> Oligonucleotide primer

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<400> 16
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<221> misc_feature
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<223> n = A,T,C or G

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<223> n = A,T,C or G

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<210> 19
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<220>
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<400> 19
tgyaartayg aytwygt 17

<210> 20
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<400> 20
acrwartcrt ayttrca 17

<210> 21
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<221> misc_feature
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<223> n = A,T,C or G

<400> 21
ywnggnmrnt dbtgygg 17

<210> 22
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<221> misc_feature
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<223> n = A,T,C or G

<400> 22
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<221> misc_feature
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<223> n = A,T,C or G

<400> 23
tdbccnmand vntaycc 17

<210> 24
<211> 17
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<213> Artificial Sequence

<220>
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<221> misc_feature
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ggrtanbhnt knggvha 17

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<211> 20
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agcaggtcca gtggcaaagc 20

<210> 26
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<400> 26
cgtttgatga aagatttggg c 21

<210> 27
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<400> 27
ggaggtctat ataagcagag c 21

<210> 28
<211> 18
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<400> 28
taacagagga ggtaagat 18

<210> 29
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<400> 29
tcggttctct ttagttct 18

<210> 30
<211> 25
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<400> 30
tctggacgtc ctcctgctgg tatag 25

<210> 31
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ggtatggagc caggggcaag ttggg 25

<210> 32
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<400> 32
gagtggcaac ttccagggcc aggagag 27

<210> 33
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cttttgctag cctcaacccct gactatc 27

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cgcgcggttt aaacgccacc atgagcctct tcggg 35

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<400> 35
cgtatcggcg cgccctatcc tcctgtgctc cc 32

<210> 36
<211> 1882
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (226)...(1338)

<400> 36
ccgtcaccat ttatcagctc agcaccacaa ggaagtgcgg cacccacacg cgctcggaaa 60
gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc cgggccagcg 120
cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac 180
ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc 237
Met His Arg Leu
1

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atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac     285
Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp
 5                  10                  15                  20

act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc     333
Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala
                25                  30                  35

aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga     381
Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg
            40                  45                  50

gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga     429
Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg
        55                  60                  65

ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac     477
Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His
    70                  75                  80

tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga     525
Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly
85                  90                  95                 100

tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt     573
Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val
                105                 110                 115

gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga     621
Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly
            120                 125                 130

cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa     669
His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys
        135                 140                 145

atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag     717
Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys
    150                 155                 160
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att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag     765
Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu
165                 170                 175                 180

acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac     813
Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn
                185                 190                 195

tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa     861
Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys
            200                 205                 210

aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat     909
Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn
        215                 220                 225

cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct     957
Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro
    230                 235                 240

cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg    1005
Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu
245                 250                 255                 260

gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat    1053
Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn
                265                 270                 275

tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc    1101
Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe
            280                 285                 290

ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt    1149
Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys
        295                 300                 305

gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg    1197
Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val
    310                 315                 320

aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg    1245
Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg
325                 330                 335                 340
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agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg agggtgagat 1398
aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca 1518
tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga ggttatatat 1578
gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa tgtttttttt 1638
ttttggtata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa 1698
tcctttgcca aaataaggga tggtcaaata tatgaaacat gtctttagaa aatttaggag 1758
ataaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa 1818
agcatcttgt atattaaaaa tcaaaagatg aggctttctt acatatacat cttagttgat 1878
tatt 1882

<210> 37
<211> 370
<212> PRT
<213> Homo sapiens

<400> 37
Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
1 5 10 15
Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
20 25 30
Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
35 40 45
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
50 55 60
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65 70 75 80
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
85 90 95
Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
100 105 110
Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
115 120 125

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Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
    130                 135                 140
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145                 150                 155                 160
Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
                165                 170                 175
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
            180                 185                 190
Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
        195                 200                 205
Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
    210                 215                 220
Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
225                 230                 235                 240
Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
                245                 250                 255
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
            260                 265                 270
Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
        275                 280                 285
Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
    290                 295                 300
Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
305                 310                 315                 320
Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
                325                 330                 335
His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
            340                 345                 350
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
        355                 360                 365
Pro Arg
    370
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<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC21,222

<400> 38
tgagccctcg ccccagtcag 20

<210> 39
<211> 25
<212> DNA
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<220>
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<400> 39
acatacagga aagccttgcc caaaa 25

<210> 40
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<220>
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<400> 40
aaactaccct gcgattctct gctgc 25

<210> 41
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<212> DNA
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<220>
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<400> 41
ggtaaatgga gcttggctga g 21

<210> 42
<211> 3571
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1049)...(2086)

<400> 42

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ctgcgccagc acctgttggc ccgccagctg gccgcccgcg ccccccgcgc ccccccgcgc    180
cgcccggccg ccagccccgc gccccgcgcg ccgcccgctg ggggaaagtg gagacgggga    240
ggggacaaga gcgatcctcc aggccagcca ggccttccct tagccgcccg tgcttagccg    300
ccacctctcc tcagccctgc gtcctgccct gccttagggc aggcatccga gcgctcgcga    360
ctccgagccg cccaagctct cccggcttcc cgcagcactt cgccggtacc cgagggaact    420
tcggtggcca ccgactgcag caaggaggag gctccgcggt ggatccgggc cagtcccgag    480
tcgtccccgc ggcctctctg cccgcccggg acccgcgcgg cactcgcagg gcacggtccc    540
ctccccccag gtgggggtgg ggcgccgcct gccgccccga tcagcagctt tgtcattgat    600
cccaaggtgc tcgcctcgct gccgacctgg cttccagtct ggcttggcgg gaccccgagt    660
cctcgcctgt gtcctgtccc ccaaactgac aggtgctccc tgcgagtcgc cacgactcat    720
cgccgctccc ccgcgtcccc acccttctt tcctccctcg cctaccccca ccccccgcac    780
ttcggcacag ctcaggattt gtttaaacct tgggaaactg gttcaggtcc aggttttgct    840
ttgatccttt tcaaaaactg gagacacaga agagggctct aggaaaaact tttggatggg    900
attatgtgga aactaccctg cgattctctg ctgccagagc cggccaggcg cttccaccgc    960
agcgcagcct ttccccggct gggctgagcc ttggagtcgt cgcttcccca gtgcccgccg   1020
cgagtgagcc ctcgccccag tcagccaa atg ctc ctc ctc ggc ctc ctc ctg      1072
                                 Met Leu Leu Leu Gly Leu Leu Leu
                                  1               5

ctg aca tct gcc ctg gcc ggc caa aga acg ggg act cgg gct gag tcc     1120
Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser
     10.                 15                  20

aac ctg agc agc aag ttg cag ctc tcc agc gac aag gaa cag aac gga     1168
Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly
 25                  30                  35                  40

gtg caa gat ccc cgg cat gag aga gtt gtc act ata tct ggt aat ggg     1216
Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly
                 45                  50                  55

agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg     1264
Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val
             60                  65                  70

ctg gtg tgg aga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg     1312
Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu
         75                  80                  85
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aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc      1360
Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys
     90                  95                 100

aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta      1408
Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu
105                 110                 115                 120

gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa      1456
Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys
                125                 130                 135

gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct      1504
Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser
            140                 145                 150

gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca      1552
Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr
        155                 160                 165

gaa acc acg agt cct tcg gtg ttg ccc cct tca tct ttg tca ttg gac      1600
Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp
    170                 175                 180

ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att      1648
Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile
185                 190                 195                 200

cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac      1696
Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr
                205                 210                 215

aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa      1744
Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys
            220                 225                 230

agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac      1792
Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr
        235                 240                 245

agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag      1840
Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys
    250                 255                 260
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agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt 1888
Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys
265 270 275 280

gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt 1936
Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys
285 290 295

gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga 1984
Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg
300 305 310

cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct 2032
Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala
315 320 325

ctg gaa cac cac gag gaa tgt gac tgt gtg tgt aga gga aac gca gga 2080
Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Asn Ala Gly
330 335 340

ggg taa ctgcagcctt cgtagcagca cacgtgagca ctggcattct gtgtaccccc 2136
Gly *
345

acaagcaacc ttcatcccca ccagcgttgg ccgcagggct ctcagctgct gatgctggct 2196
atggtaaaga tcttactcgt ctccaaccaa attctcagtt gtttgcttca atagccttcc 2256
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actgtactat catcaattcc caattctgtt cttagagcta cgaacagaac agagcttgag 3156
taaatatgga gccattgcta acctacccct ttctatggga aataggagta tagctcagag 3216

aagcacgtcc ccagaaacct cgaccatttc taggcacagt gttctgggct atgctgcgct 3276
gtatggacat atcctattta tttcaatact agggttttat tacctttaaa ctctgctcca 3336
tacacttgta ttaatacatg gatattttta tgtacagaag tatatcattt aaggagttca 3396
cttattatac tctttggcaa ttgcaaagaa aatcaacata atacattgct tgtaaatgct 3456
taatctgtgc ccaagttttg tggtgactat ttgaattaaa atgtattgaa tcatcaaata 3516
aaataatctg gctattttgg ggaaaaaaaa aaaaaaaaaa aaaaagggcg gccgc 3571

<210> 43
<211> 345
<212> PRT
<213> Mus musculus

<400> 43
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Arg Thr Gly Thr Arg Ala Glu Ser Asn Leu Ser Ser Lys Leu Gln Leu
20 25 30
Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
35 40 45
Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
50 55 60
His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
65 70 75 80
Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
85 90 95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
100 105 110
Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
115 120 125
Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
130 135 140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145 150 155 160
Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu
165 170 175
Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala
180 185 190
Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
195 200 205
Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
210 215 220
Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu
225 230 235 240

Leu Lys Glu Glu Val Lys Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
245 250 255
Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
260 265 270
Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
275 280 285
His Asn Cys Asn Glu Cys Gln Cys Val Pro Arg Lys Val Thr Lys Lys
290 295 300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu
305 310 315 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
325 330 335
Cys Val Cys Arg Gly Asn Ala Gly Gly
340 345

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<211> 65
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<223> oligonucleotide primer ZC20,572

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ggcgg 65

<210> 45
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
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tgcac 65

<210> 46
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
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<400> 46
tgtcgatgaa gccctgaaag acgcgcagac taattcgagc 40

<210> 47
<211> 60
<212> DNA
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<220>
<223> oligonucleotide primer ZC19,351

<400> 47
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<210> 48
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<220>
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<400> 48
actcactata gggcgaattg cccgggggat ccacgcggaa ccagcggtac cgaattcgcg 60

<210> 49
<211> 42
<212> DNA
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<220>
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<400> 49
acggccagtg aattgtaata cgactcacta tagggcgaat tg 42

<210> 50
<211> 1095
<212> DNA

<213> Artificial Sequence

<220>
<223> Fused DNA

<400> 50

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agtaaattcc agttttccag caacaaggaa cagaacggag tacaagatcc tcagcatgag     180
agaattatta ctgtgtctac taatggaagt attcacagcc caaggtttcc tcatacttat     240
ccaagaaata cggtcttggt atggagatta gtagcagtag aggaaaatgt atggatacaa     300
cttacgtttg atgaaagatt tgggcttgaa gacccagaag atgacatatg caagtatgat     360
tttgtagaag ttgaggaacc cagtgatgga actatattag ggcgctggtg tggttctggt     420
actgtaccag gaaaacagat ttctaaagga aatcaaatta ggataagatt tgtatctgat     480
gaatattttc cttctgaacc agggttctgc atccactaca acattgtcat gccacaattc     540
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aatgctataa ctgcctttag taccttggaa gaccttattc gatatcttga accagagaga     660
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gtttttggaa gaaaatccag agtggtggat ctgaaccttc taacagagga ggtaagatta     780
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